

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel G Protein Coupled Receptor Protein and Its Use

<130> A99137

5 <150> JP 10-207579

<151> 1998-07-23

<150> JP 10-225060

<151> 1998-08-07

<150> JP 10-284328

10 <151> 1998-10-06

<160> 6

<210> 1

<211> 872

<212> PRT

15 <213> Human

<400> 1

Ala Glu Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr Tyr Ser

1

5

10

15

Val Arg Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln Leu Arg

20

20

25

30

09744226-012004
FOI b7D b7C b7E

	Asn	Leu	Thr	Pro	Gly	Gly	Lys	Asp	Ser	Ala	Ala	Arg	Ser	Leu	Asn	Lys
	35				40				45							
	Ala	Met	Val	Glu	Thr	Val	Asn	Asn	Leu	Leu	Gln	Pro	Gln	Ala	Leu	Asn
	50				55				60							
5	Ala	Trp	Arg	Asp	Leu	Thr	Thr	Ser	Asp	Gln	Leu	Arg	Ala	Ala	Thr	Met
	65				70				75				80			
	Leu	Leu	His	Thr	Val	Glu	Glu	Ser	Ala	Phe	Val	Leu	Ala	Asp	Asn	Leu
	85				90				95							
	Leu	Lys	Thr	Asp	Ile	Val	Arg	Glu	Asn	Thr	Asp	Asn	Ile	Lys	Leu	Glu
10	100				105				110							
	Val	Ala	Arg	Leu	Ser	Thr	Glu	Gly	Asn	Leu	Glu	Asp	Leu	Lys	Phe	Pro
	115				120				125							
	Glu	Asn	Met	Gly	His	Gly	Ser	Thr	Ile	Gln	Leu	Ser	Ala	Asn	Thr	Leu
	130				135				140							
15	Lys	Gln	Asn	Gly	Arg	Asn	Gly	Glu	Ile	Arg	Val	Ala	Phe	Val	Leu	Tyr
	145				150				155				160			
	Asn	Asn	Leu	Gly	Pro	Tyr	Leu	Ser	Thr	Glu	Asn	Ala	Ser	Met	Lys	Leu
	165				170				175							
	Gly	Thr	Glu	Ala	Leu	Ser	Thr	Asn	His	Ser	Val	Ile	Val	Asn	Ser	Pro
20	180				185				190							
	Val	Ile	Thr	Ala	Ala	Ile	Asn	Lys	Glu	Phe	Ser	Asn	Lys	Val	Tyr	Leu
	195				200				205							
	Ala	Asp	Pro	Val	Val	Phe	Thr	Val	Lys	His	Ile	Lys	Gln	Ser	Glu	Glu
	210				215				220							
25	Asn	Phe	Asn	Pro	Asn	Cys	Ser	Phe	Trp	Ser	Tyr	Ser	Lys	Arg	Thr	Met

	225					230						235					240
	Thr	Gly	Tyr	Trp	Ser	Thr	Gln	Gly	Cys	Arg	Leu	Leu	Thr	Thr	Asn	Lys	
						245						250					255
	Thr	His	Thr	Thr	Cys	Ser	Cys	Asn	His	Leu	Thr	Asn	Phe	Ala	Val	Leu	
5					260					265						270	
	Met	Ala	His	Val	Glu	Val	Lys	His	Ser	Asp	Ala	Val	His	Asp	Leu	Leu	
					275					280					285		
	Leu	Asp	Val	Ile	Thr	Trp	Val	Gly	Ile	Leu	Leu	Ser	Leu	Val	Cys	Leu	
					290					295					300		
10	Leu	Ile	Cys	Ile	Phe	Thr	Phe	Cys	Phe	Phe	Arg	Gly	Leu	Gln	Ser	Asp	
	305					310					315					320	
	Arg	Asn	Thr	Ile	His	Lys	Asn	Leu	Cys	Ile	Ser	Leu	Phe	Val	Ala	Glu	
					325						330					335	
	Leu	Leu	Phe	Leu	Ile	Gly	Ile	Asn	Arg	Thr	Asp	Gln	Pro	Ile	Ala	Cys	
15					340					345					350		
	Ala	Val	Phe	Ala	Ala	Leu	Leu	His	Phe	Phe	Phe	Leu	Ala	Ala	Phe	Thr	
					355					360					365		
	Trp	Met	Phe	Leu	Glu	Gly	Val	Gln	Leu	Tyr	Ile	Met	Leu	Val	Glu	Val	
					370					375					380		
20	Phe	Glu	Ser	Glu	His	Ser	Arg	Arg	Lys	Tyr	Phe	Tyr	Leu	Val	Gly	Tyr	
	385					390					395					400	
	Gly	Met	Pro	Ala	Leu	Ile	Val	Ala	Val	Ser	Ala	Ala	Val	Asp	Tyr	Arg	
					405						410					415	
	Ser	Tyr	Gly	Thr	Asp	Lys	Val	Cys	Trp	Leu	Arg	Leu	Asp	Thr	Tyr	Phe	
25					420					425						430	

09744226-012201

Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val

435

440

445

Ile Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile

450

455

460

5 Leu Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile

465

470

475

480

Gly Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly

485

490

495

Leu Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr

10

500

505

510

Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val

515

520

525

Leu Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His

530

535

540

15

Cys Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr

545

550

555

560

Ser Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg

565

570

575

Ile Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser

20

580

585

590

Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly

595

600

605

Leu Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu

610

615

620

25

Asn Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Ser Gly Glu Tyr Leu

09744226-012201

	625	630	635	640
	Ser Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr			
	645	650	655	
	Ala Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro			
5	660	665	670	
	Ser Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Leu			
	675	680	685	
	Met Asn Lys Leu Val Asn Asn Leu Gly Ser Gly Arg Glu Asp Asp Ala			
	690	695	700	
10	Ile Val Leu Asp Asp Ala Thr Ser Phe Asn His Glu Glu Ser Leu Gly			
	705	710	715	720
	Leu Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg			
	725	730	735	
	Val Tyr Ser Thr Glu Asn His Gln Pro His His Tyr Thr Arg Arg Arg			
15	740	745	750	
	Ile Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asn Glu			
	755	760	765	
	His Thr Glu Asp Leu Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser			
	770	775	780	
20	Met Pro Thr Leu Ala Gly Val Ala Ala Thr Glu Ser Val Thr Thr Ser			
	785	790	795	800
	Thr Gln Thr Glu Pro Pro Pro Ala Lys Cys Gly Asp Ala Glu Asp Val			
	805	810	815	
	Tyr Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Gln			
25	820	825	830	

Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile

835

840

845

Val Pro Pro Asn Lys Asp Gly Thr Pro Pro Glu Gly Ser Ser Lys Gly

850

855

860

5 Pro Ala His Leu Val Thr Ser Leu

865

870

<210> 2

<211> 2616

<212> DNA

10 <213> Human

<400> 2

GCTGAACAGA CAAGAAATCA CTTGAATGCT GGGGACATCA CCTACTCTGT CCGGGCCATG 60

GACCAGCTGG TAGGCCTCCT AGATGTACAG CTTCGGAAC TGAACCCAGG TGGAAAAGAT 120

AGTGCTGCCC GGAGTTTGAA CAAGGCAATG GTCGAGACAG TTAACAACCT CCTTCAGCCA 180

15 CAAGCTTTGA ATGCATGGAG AGACCTGACT ACGAGTGATC AGCTGCGTGC GGCCACCATG 240

TTGCTTCATA CTGTGGAGGA AAGTGCTTTT GTGCTGGCTG ATAACCTTTT GAAGACTGAC 300

ATTGTCAGGG AGAATACAGA CAATATTAAA TTGGAAGTTG CAAGACTGAG CACAGAAGGA 360

AACTTAGAAG ACCTAAAATT TCCAGAAAAC ATGGGCCATG GAAGCACTAT CCAGCTGTCT 420

GCAAATACCT TAAAGCAAAA TGGCCGAAAT GGAGAGATCA GAGTGGCCTT TGTCTGTAT 480

20 AACAAC TTGG GTCCTTATTT ATCCACGGAG AATGCCAGTA TGAAGTTGGG AACGGAAGCT 540

TTGTCCACAA ATCATTCTGT TATTGTCAAT TCCCCTGTTA TTACGGCAGC AATAAACAAA 600

GAGTTCAGTA ACAAGGTTTA TTTGGCTGAT CCTGTGGTAT TTAAGTTTAA ACATATCAAG 660

CAGTCAGAGG AAAATTTCAA CCCTAACTGT TCATTTTGA GCTACTCCAA GCGTACAATG 720

ACAGGTTATT GGTCAACACA AGGCTGTCGG CTCCTGACAA CAAATAAGAC ACATACTACA 780

25 TGCTCTTGTA ACCACCTAAC AAATTTTGCA GTACTGATGG CACATGTGGA AGTTAAGCAC 840

AGTGATGCGG TCCATGACCT CCTTCTGGAT GTGATCACGT GGGTTGGAAT TTTGCTGTCC 900
 CTTGTTTGTC TCCTGATTTG CATCTTCACA TTTTGCTTTT TCCGCGGGCT CCAGAGTGAC 960
 CGTAACACCA TCCACAAGAA CCTCTGCATC AGTCTCTTTG TAGCAGAGCT GCTCTTCCTG 1020
 ATTGGGATCA ACCGAACTGA CCAACCAATT GCCTGTGCTG TTTTCGCTGC CCTGTTTTCT 1080
 5 TCTTCTTGGC TGCCTTCACC TGGATGTTCC TGGAGGGGGT GCAGCTTTAT ATACATCATG 1140
 CTGGTGGAGG TTTTGAGAG TGAACATTCA CGTAGGAAAT ACTTTTATCT GGTGCGCTAT 1200
 GGGATGCCTG CACTCATTGT GGCTGTGTCA GCTGCAGTAG ACTACAGGAG TTATGGAACA 1260
 GATAAAGTAT GTTGGCTCCG ACTTGACACC TACTTCATTT GGAGTTTTAT AGGACCAGCA 1320
 ACTTTGATAA TTATGCTTAA TGTAATCTTC CTGGGATTG CTTTATATAA AATGTTTCAT 1380
 10 CATACTGCTA TACTGAAACC TGAATCAGGC TGTCTTGATA ACATCAAGTC ATGGGTTATA 1440
 GGTGCAATAG CTCTTCTCTG CCTATTAGGA TTGACCTGGG CCTTTGGA CTATGTATATT 1500
 AATGAAAGCA CAGTCATCAT GGCCTATCTC TTCACCATTT TCAATTCTCT ACAGGGAATG 1560
 TTTATATTTA TTTTCCATTG TGTCTACAG AAGAAGGTAC GAAAAGAGTA TGGGAAATGC 1620
 CTGCGAACAC ATTGCTGTAG TGGCAAAAGT ACAGAGAGTT CCATTGGTTC AGGGAAAACA 1680
 15 TCTGGTTCTC GAACTCCTGG ACGCTACTCC ACAGGCTCAC AGAGCCGAAT CCGTAGAATG 1740
 TGGAATGACA CGGTCGAAA GCAGTCAGAG TCTTCCTTTA TTAGTGAGA CATAAACAGT 1800
 TCAGCGTCAC TCAACAGAGA GGGGCTTCTG AACAAATGCCA GGGATACAAG TGTCATGGAT 1860
 ACTCTACCAC TGAATGGTAA CCATGGCAAT AGTTACAGCA TTGCCAGCGG CGAATACCTG 1920
 AGCAACTGTG TGCAAATCAT AGACCGTGGC TATAACCATA ACGAGACCGC CCTAGAGAAA 1980
 20 AAGATTCTGA AGGAACTCAC TTCCAATAT ATCCCTTCTT ACCTGAACAA CCATGAGCGC 2040
 TCCAGTGAAC AGAACAGGAA TCTGATGAAC AAGCTGGTGA ATAACTTGG CAGTGGAAGG 2100
 GAAGATGATG CCATTGTCCT GGATGATGCC ACCTCGTTTA ACCACGAGGA GAGTTGGGC 2160
 CTGGAATCA TTCATGAGGA ATCTGATGCT CCTTTGCTGC CCCCAGAGT AACTCCACC 2220
 GAGAACCACC AGCCACACCA TTATACCAGA AGGCGGATCC CCCAAGACCA CAGTGAGAGC 2280
 25 TTTTCCCTT TGCTAACCA CGAGCACACA GAAGATCTCC AGTCACCCCA TAGAGACTCT 2340

CTCTATACCA GCATGCCGAC ACTGGCTGGT GTGGCCGCCA CAGAGAGTGT TACCACCAGC 2400
 ACCCAGACCG AACCCCCACC GGCCAAATGT GGTGATGCCG AAGATGTTTA CTACAAAAGC 2460
 ATGCCAAACC TAGGCTCCAG AAACCACGTC CATCAGCTGC ATACTTACTA CCAGCTAGGT 2520
 CGCGGCAGCA GTGATGGATT TATAGTTCCT CCAAACAAAG ATGGGACCCC TCCCGAGGGA 2580
 5 AGTTCAAAAG GACCGGCTCA TTTGGTCACT AGTCTA 2616

<210> 3

<211> 1021

<212> PRT

<213> Human

10 <400> 3

Glu Gly Ser Lys Gly Thr Lys Pro Pro Pro Ala Val Ser Thr Thr Lys

1 5 10 15

Ile Pro Pro Ile Thr Asn Ile Phe Pro Leu Pro Glu Arg Phe Cys Glu

20 25 30

15 Ala Leu Asp Ser Lys Gly Ile Lys Trp Pro Gln Thr Gln Arg Gly Met

35 40 45

Met Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Thr Ala Ser Tyr

50 55 60

Leu Cys Met Ile Ser Thr Gly Thr Trp Asn Pro Lys Gly Pro Asp Leu

20 65 70 75 80

Ser Asn Cys Thr Ser His Trp Val Asn Gln Leu Ala Gln Lys Ile Arg

85 90 95

Ser Gly Glu Asn Ala Ala Ser Leu Ala Asn Glu Leu Ala Lys His Thr

100 105 110

25 Lys Gly Pro Val Phe Ala Gly Asp Val Ser Ser Ser Val Arg Leu Met

09744226-012201

	115	120	125	
	Glu Gln Leu Val Asp Ile Leu Asp Ala Gln Leu Gln Glu Leu Lys Pro			
	130	135	140	
	Ser Glu Lys Asp Ser Ala Gly Arg Ser Tyr Asn Lys Leu Gln Lys Arg			
5	145	150	155	160
	Glu Lys Thr Cys Arg Ala Tyr Leu Lys Ala Ile Val Asp Thr Val Asp			
	165	170	175	
	Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys His Met Asn Ser			
	180	185	190	
10	Ser Glu Gln Ala His Thr Ala Thr Met Leu Leu Asp Thr Leu Glu Glu			
	195	200	205	
	Gly Ala Phe Val Leu Ala Asp Asn Leu Leu Glu Pro Thr Arg Val Ser			
	210	215	220	
	Met Pro Thr Glu Asn Ile Val Leu Glu Val Ala Val Leu Ser Thr Glu			
15	225	230	235	240
	Gly Gln Ile Gln Asp Phe Lys Phe Pro Leu Gly Ile Lys Gly Ala Gly			
	245	250	255	
	Ser Ser Ile Gln Leu Ser Ala Asn Thr Val Lys Gln Asn Ser Arg Asn			
	260	265	270	
20	Gly Leu Ala Lys Leu Val Phe Ile Ile Tyr Arg Ser Leu Gly Gln Phe			
	275	280	285	
	Leu Ser Thr Glu Asn Ala Thr Ile Lys Leu Gly Ala Asp Phe Ile Gly			
	290	295	300	
	Arg Asn Ser Thr Ile Ala Val Asn Ser His Val Ile Ser Val Ser Ile			
25	305	310	315	320

SECRET

335

350

365

380

400

415

430

445

460

480

495

510

25

	515	520	525.
	Val Ser Ala Ala Ile Asp Tyr Lys Ser Tyr Gly Thr Glu Lys Ala Cys		
	530	535	540
	Trp Leu His Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile Gly Pro Val		
5	545	550	555
	Thr Phe Ile Ile Leu Leu Asn Ile Ile Phe Leu Val Ile Thr Leu Cys		
	565	570	575
	Lys Met Val Lys His Ser Asn Thr Leu Lys Pro Asp Ser Ser Arg Leu		
	580	585	590
10	Glu Asn Ile Lys Ser Trp Val Leu Gly Ala Phe Ala Leu Leu Cys Leu		
	595	600	605
	Leu Gly Leu Thr Trp Ser Phe Gly Leu Leu Phe Ile Asn Glu Glu Thr		
	610	615	620
	Ile Val Met Ala Tyr Leu Phe Thr Ile Phe Asn Ala Phe Gln Gly Val		
15	625	630	635
	Phe Ile Phe Ile Phe His Cys Ala Leu Gln Lys Lys Val Arg Lys Glu		
	645	650	655
	Tyr Gly Lys Cys Phe Arg His Ser Tyr Cys Cys Gly Gly Leu Pro Thr		
	660	665	670
20	Glu Ser Pro His Ser Ser Val Lys Ala Ser Thr Thr Arg Thr Ser Ala		
	675	680	685
	Arg Tyr Ser Ser Gly Thr Gln Ser Arg Ile Arg Arg Met Trp Asn Asp		
	690	695	700
	Thr Val Arg Lys Gln Ser Glu Ser Ser Phe Ile Ser Gly Asp Ile Asn		
25	705	710	715
			720

	Ser Thr Ser Thr Leu Asn Gln Gly Met Thr Gly Asn Tyr Leu Leu Thr			
	725	730	735	
	Asn Pro Leu Leu Arg Pro His Gly Thr Asn Asn Pro Tyr Asn Thr Leu			
	740	745	750	
5	Leu Ala Glu Thr Val Val Cys Asn Ala Pro Ser Ala Pro Val Phe Asn			
	755	760	765	
	Ser Pro Gly His Ser Leu Asn Asn Ala Arg Asp Thr Ser Ala Met Asp			
	770	775	780	
	Thr Leu Pro Leu Asn Gly Asn Phe Asn Asn Ser Tyr Ser Leu His Lys			
10	785	790	795	800
	Gly Asp Tyr Asn Asp Ser Val Gln Val Val Asp Cys Gly Leu Ser Leu			
	805	810	815	
	Asn Asp Thr Ala Phe Glu Lys Met Ile Ile Ser Glu Leu Val His Asn			
	820	825	830	
15	Asn Leu Arg Gly Ser Ser Lys Thr His Asn Leu Glu Leu Thr Leu Pro			
	835	840	845	
	Val Lys Pro Val Ile Gly Gly Ser Ser Ser Glu Asp Asp Ala Ile Val			
	850	855	860	
	Ala Asp Ala Ser Ser Leu Met His Ser Asp Asn Pro Gly Leu Glu Leu			
20	865	870	875	880
	His His Lys Glu Leu Glu Ala Pro Leu Ile Pro Gln Arg Thr His Ser			
	885	890	895	
	Leu Leu Tyr Gln Pro Gln Lys Lys Val Lys Ser Glu Gly Thr Asp Ser			
	900	905	910	
25	Tyr Val Ser Gln Leu Thr Ala Glu Ala Glu Asp His Leu Gln Ser Pro			

	915	920	925
	Asn Arg Asp Ser Leu Tyr Thr Ser Met Pro Asn Leu Arg Asp Ser Pro		
	930	935	940
	Tyr Pro Glu Ser Ser Pro Asp Met Glu Glu Asp Leu Ser Pro Ser Arg		
5	945	950	955
	Arg Ser Glu Asn Glu Asp Ile Tyr Tyr Lys Ser Met Pro Asn Leu Gly		
	965	970	975
	Ala Gly His Gln Leu Gln Met Cys Tyr Gln Ile Ser Arg Gly Asn Ser		
	980	985	990
10	Asp Gly Tyr Ile Ile Pro Ile Asn Lys Glu Gly Cys Ile Pro Glu Gly		
	995	1000	1005
	Asp Val Arg Glu Gly Gln Met Gln Leu Val Thr Ser Leu		
	1010	1015	1020
	<210> 4		
15	<211> 3063		
	<212> DNA		
	<213> Human		
	<400> 4		
	GAAGGAAGCA AAGGGACAAA ACCACCTCCA GCAGTTTCTA CAACCAAAAT TCCACCTATA	60	
20	ACAAATATTT TTCCCTGCC AGAGAGATTC TGTGAAGCAT TAGACTCCAA GGGGATAAAG	120	
	TGGCCTCAGA CACAAAGGGG AATGATGGTT GAACGACCAT GCCCTAAGGG AACAAGAGGA	180	
	ACTGCCTCAT ATCTCTGCAT GATTTCCTACT GGAACATGGA ACCCTAAGGG CCCCATCTT	240	
	AGCAACTGTA CCTCAGCTG GGTGAATCAG CTGGCTCAGA AGATCAGAAG CGGAGAAAAT	300	
	GCTGCTAGTC TTGCCAATGA ACTGGCTAAA CATAACAAAG GGCCAGTGTT TGCTGGGGAT	360	
25	GTAAGTTCTT CAGTGAGATT GATGGAGCAG TTGGTGGACA TCCTTGATGC ACAGCTGCAG	420	

GAACTGAAAC CTAGTGAAAA AGATTCAGCT GGACGGAGTT ATAACAAGCT CAAAAACGA 480
 GAGAAGACAT GCAGGGCTTA CCTTAAGGCA ATTGTTGACA CAGTGGACAA CTTCTGAGA 540
 CCTGAAGCTT TGGAATCATG GAAACATATG AATTCTTCTG AACAAGCACA TACTGCAACA 600
 ATGTTACTCG ATACATTGGA AGAAGGAGCT TTTGTCCTAG CTGACAATCT TTTAGAACCA 660
 5 ACAAGGGTCT CAATGCCAC AGAAAATATT GTCCTGGAAG TTGCCGTACT CAGTACAGAA 720
 GGACAGATCC AAGACTTTAA ATTTCTCTG GGCATCAAAG GAGCAGGCAG CTCAATCCAA 780
 CTGTCCGCAA ATACCGTCAA ACAGAACAGC AGGAATGGGC TTGCAAAGTT GGTGTTTCATC 840
 ATTTACCGGA GCCTGGGACA GTTCCTTAGT ACAGAAAATG CAACCATTAA ACTGGGTGCT 900
 GATTTTATTG GTCGTAATAG CACCATTGCA GTGAACTCTC ACGTCATTTT AGTTTCAATC 960
 10 AATAAGAGT CCAGCCGAGT ATACCTGACT GATCCTGTGC TTTTACCCT GCCACACATT 1020
 GATCCTGACA ATTATTCAA TGCAAAGTGC TCCTTCTGGA ACTACTCAGA GAGAACTATG 1080
 ATGGGATATT GGTCTACCCA GGGCTGCAAG CTGGTTGACA CTAATAAAAC TCGAACAACG 1140
 TGTGCATGCA GCCACCTAAC CAATTTTGCA ATTCTCATGG CCCACAGGGA AATTGCATAT 1200
 AAAGATGGCG TTCATGAATT ACTTCTTACA GTCATCACCT GGGTGGGAAT TGTCATTTCC 1260
 15 CTTGTTTGCC TGGCTATCTG CATCTTACC TTCTGCTTTT TCCGTGGCCT ACAGAGTGAC 1320
 CGAAATACTA TTCACAAGAA CCTTTGTATC AACCTTTTCA TTGCTGAATT TATTTTCTTA 1380
 ATAGGCATTG ATAAGACAAA ATATGCGATT GCATGCCCAA TATTTGCAGG ACTTCTACAC 1440
 TTTTCTTTT TGGCAGCTTT TGCTTGATG TGCCTAGAAG GTGTGCAGCT CTACCTAATG 1500
 TTAGTTGAAG TTTTGAAG TGAATATTCA AGGAAAAAAT ATTACTATGT TGCTGGTTAC 1560
 20 TTGTTTCCTG CCACAGTGGT TGGAGTTTCA GCTGCTATTG ACTATAAGAG CTATGGAACA 1620
 GAAAAAGCTT GCTGGCTTCA TGTGATAAC TACTTTATAT GGAGCTTCAT TGGACCTGTT 1680
 ACCTTCATTA TTCTGCTAAA TATTATCTTC TTGGTGATCA CATTGTGCAA AATGGTGAAG 1740
 CATTCAAACA CTTTGAAACC AGATTCTAGC AGGTTGAAA ACATTAAGTC TTGGGTGCTT 1800
 GCGCTTTTCG CTCTTCTGTG TCTTCTGGC CTCACCTGGT CCTTTGGGT GCTTTTATT 1860
 25 AATGAGGAGA CTATTGTGAT GGCATATCTC TTTACTATAT TTAATGCTTT CCAGGGAGTG 1920

TTCATTTTCA TCTTTCAGTG TGCTCTCCAA AAGAAAGTAC GAAAAGAATA TGGCAAGTGC 1980
 TTCAGACACT CATACTGCTG TGGAGGCCTC CCAACTGAGA GTCCCCACAG TTCAGTGAAG 2040
 GCATCAACCA CCAGAACCAG TGCTCGCTAT TCCTCTGGCA CACAGAGTCG TATAAGAAGA 2100
 ATGTGGAATG ATACTGTGAG AAAACAATCA GAATCTTCTT TTATCTCAGG TGACATCAAT 2160
 5 AGCACTTCAA CACTTAATCA AGGAATGACT GGCAATTACC TACTAACAAA CCCTCTTCTT 2220
 CGACCCACAG GCACTAACAA CCCCTATAAC ACATTGCTCG CTGAAACAGT TGTATGTAAT 2280
 GCCCCTTCAG CTCCTGTATT TAACTACCA GGACATTAC TGAACAATGC CAGGGATACA 2340
 AGTGCCATGG ATACTCTACC GCTAAATGGT AATTTTAACA ACAGCTACTC GCTGCACAAG 2400
 GGTGACTATA ATGACAGCGT GCAAGTTGTG GACTGTGGAC TAAGTCTGAA TGATACTGCT 2460
 10 TTTGAGAAAA TGATCATTTT AGAATTAGTG CACAACAAC TACGGGGCAG CAGCAAGACT 2520
 CACAACCTCG AGCTCAGCT ACCAGTCAA CCTGTGATTG GAGGTAGCAG CAGTGAAGAT 2580
 GATGCTATTG TGGCAGATGC TTCATCTTTA ATGCACAGCG ACAACCCAGG GCTGGAGCTC 2640
 CATCACAAG AACTCGAGGC ACCACTTATT CCTCAGCGGA CTCCTCCCT TCTGTACCA 2700
 CCCCAGAAGA AAGTGAAGTC CGAGGGAAC TACAGCTATG TCTCCCACT GACAGCAGAG 2760
 15 GCTGAAGATC ACCTACAGTC CCCCAACAGA GACTCTCTTT ATACAAGCAT GCCCAATCTT 2820
 AGAGACTCTC CCTATCCGA GAGCAGCCCT GACATGGAAG AAGACCTCTC TCCCTCCAGG 2880
 AGGAGTGAGA ATGAGGACAT TTAATAAAA AGCATGCCAA ATCTTGAGC TGGCCATCAG 2940
 CTTCAGATGT GCTACCAGAT CAGCAGGGGC AATAGTGATG GTTATATAAT CCCCATTAAC 3000
 AAAGAAGGGT GTATTCCAGA AGGAGATGTT AGAGAAGGAC AAATGCAGCT GGTTACAAG 3060
 20 CTT 3063

<210> 5

<211> 1474

<212> PRT

<213> Human

25 <400> 5

Deleuze

10

20

25

35

40

50

55

10

65

70

75

85

90

100

105

115

120

130

135

20

145

150

155

165

170

180

185

101

09744226-012201

	195	200	205
	Asn Arg Val Asp Gly Thr Gly Phe Val Val Tyr Asp Gly Ala Val Phe		
	210	215	220
	Tyr Asn Lys Glu Arg Thr Arg Asn Ile Val Lys Tyr Asp Leu Arg Thr		
5	225	230	235
	Arg Ile Lys Ser Gly Glu Thr Val Ile Asn Thr Ala Asn Tyr His Asp		
	245	250	255
	Thr Ser Pro Tyr Arg Trp Gly Gly Lys Thr Asp Ile Asp Leu Ala Val		
	260	265	270
10	Asp Glu Asn Gly Leu Trp Val Ile Tyr Ala Thr Glu Gly Asn Asn Gly		
	275	280	285
	Arg Leu Val Val Ser Gln Leu Asn Pro Tyr Thr Leu Arg Phe Glu Gly		
	290	295	300
	Thr Trp Glu Thr Gly Tyr Asp Lys Arg Ser Ala Ser Asn Ala Phe Met		
15	305	310	315
	Val Cys Gly Val Leu Tyr Val Leu Arg Ser Val Tyr Val Asp Asp Asp		
	325	330	335
	Ser Glu Ala Ala Gly Asn Arg Val Asp Tyr Ala Phe Asn Thr Asn Ala		
	340	345	350
20	Asn Arg Glu Glu Pro Val Ser Leu Thr Phe Pro Asn Pro Tyr Gln Phe		
	355	360	365
	Ile Ser Ser Val Asp Tyr Asn Pro Arg Asp Asn Gln Leu Tyr Val Trp		
	370	375	380
	Asn Asn Tyr Phe Val Val Arg Tyr Ser Leu Glu Phe Gly Pro Pro Asp		
25	385	390	395
			400

09744236 012201
FO22T0 92247250

Pro Ser Ala Gly Pro Ala Thr Ser Pro Pro Leu Ser Thr Thr Thr Thr
405 410 415

Ala Arg Pro Thr Pro Leu Thr Ser Thr Ala Ser Pro Ala Ala Thr Thr
420 425 430

5 Pro Leu Arg Arg Ala Pro Leu Thr Thr His Pro Val Gly Ala Ile Asn
435 440 445

Gln Leu Gly Pro Asp Leu Pro Pro Ala Thr Ala Pro Val Pro Ser Thr
450 455 460

Arg Arg Pro Pro Ala Pro Asn Leu His Val Ser Pro Glu Leu Phe Cys
10 465 470 475 480

Glu Pro Arg Glu Val Arg Arg Val Gln Trp Pro Ala Thr Gln Gln Gly
485 490 495

Met Leu Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Ile Ala Ser
500 505 510

15 Phe Gln Cys Leu Pro Ala Leu Gly Leu Trp Asn Pro Arg Gly Pro Asp
515 520 525

Leu Ser Asn Cys Thr Ser Pro Trp Val Asn Gln Val Ala Gln Lys Ile
530 535 540

Lys Ser Gly Glu Asn Ala Ala Asn Ile Ala Ser Glu Leu Ala Arg His
20 545 550 555 560

Thr Arg Gly Ser Ile Tyr Ala Gly Asp Val Ser Ser Ser Val Lys Leu
565 570 575

Met Glu Gln Leu Leu Asp Ile Leu Asp Ala Gln Leu Gln Ala Leu Arg
580 585 590

25 Pro Ile Glu Arg Glu Ser Ala Gly Lys Asn Tyr Asn Lys Met His Lys

09744226.012201

	595	600	605
	Arg Glu Arg Thr Cys Lys Asp Tyr Ile Lys Ala Val Val Glu Thr Val		
	610	615	620
	Asp Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys Asp Met Asn		
5	625	630	635
	Ala Thr Glu Gln Val His Thr Ala Thr Met Leu Leu Asp Val Leu Glu		
	645	650	655
	Glu Gly Ala Phe Leu Leu Ala Asp Asn Val Arg Glu Pro Ala Arg Phe		
	660	665	670
10	Leu Ala Ala Lys Glu Asn Val Val Leu Glu Val Thr Val Leu Asn Thr		
	675	680	685
	Glu Gly Gln Val Gln Glu Leu Val Phe Pro Gln Glu Glu Tyr Pro Arg		
	690	695	700
	Lys Asn Ser Ile Gln Leu Ser Ala Lys Thr Ile Lys Gln Asn Ser Arg		
15	705	710	715
	Asn Gly Val Val Lys Val Val Phe Ile Leu Tyr Asn Asn Leu Gly Leu		
	725	730	735
	Phe Leu Ser Thr Glu Asn Ala Thr Val Lys Leu Ala Gly Glu Ala Gly		
	740	745	750
20	Pro Gly Gly Pro Gly Gly Ala Ser Leu Val Val Asn Ser Gln Val Ile		
	755	760	765
	Ala Ala Ser Ile Asn Lys Glu Ser Ser Arg Val Phe Leu Met Asp Pro		
	770	775	780
	Val Ile Phe Thr Val Ala His Leu Glu Asp Lys Asn His Phe Asn Ala		
25	785	790	795
	800		

09744226-012201

	Asn Cys Ser Phe Trp Asn Tyr Ser Glu Arg Ser Met Leu Gly Tyr Trp
	805 810 815
	Ser Thr Gln Gly Cys Arg Leu Val Glu Ser Asn Lys Thr His Thr Thr
	820 825 830
5	Cys Ala Cys Ser His Leu Thr Asn Phe Ala Val Leu Met Ala His Arg
	835 840 845
	Glu Ile Tyr Gln Gly Arg Ile Asn Glu Leu Leu Leu Ser Val Ile Thr
	850 855 860
	Trp Val Gly Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Ser
10	865 870 875 880
	Thr Phe Cys Phe Leu Arg Gly Leu Gln Thr Asp Arg Asn Thr Ile His
	885 890 895
	Lys Asn Leu Cys Ile Asn Leu Phe Leu Ala Glu Leu Leu Phe Leu Val
	900 905 910
15	Gly Ile Asp Lys Thr Gln Tyr Glu Ile Ala Cys Pro Ile Phe Ala Gly
	915 920 925
	Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ser Trp Leu Cys Leu Glu
	930 935 940
	Gly Val His Leu Tyr Leu Leu Leu Val Glu Val Phe Glu Ser Glu Tyr
20	945 950 955 960
	Ser Arg Thr Lys Tyr Tyr Tyr Leu Gly Gly Tyr Cys Phe Pro Ala Leu
	965 970 975
	Val Val Gly Ile Ala Ala Ala Ile Asp Tyr Arg Ser Tyr Gly Thr Glu
	980 985 990
25	Lys Ala Cys Trp Leu Arg Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile

09744226-012201

	995	1000	1005
	Gly Pro Val Ser Phe Val Ile Val Val Asn Leu Val Phe Leu Met Val		
	1010	1015	1020
	Thr Leu His Lys Met Ile Arg Ser Ser Ser Val Leu Lys Pro Asp Ser		
5	1025	1030	1035
	Ser Arg Leu Asp Asn Ile Lys Ser Trp Ala Leu Gly Ala Ile Ala Leu		
	1045	1050	1055
	Leu Phe Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Leu Phe Ile Asn		
	1060	1065	1070
10	Lys Glu Ser Val Val Met Ala Tyr Leu Phe Thr Thr Phe Asn Ala Phe		
	1075	1080	1085
	Gln Gly Val Phe Ile Phe Val Phe His Cys Ala Leu Gln Lys Lys Val		
	1090	1095	1100
	His Lys Glu Tyr Ser Lys Cys Leu Arg His Ser Tyr Cys Cys Ile Arg		
15	1105	1110	1115
	Ser Pro Pro Gly Gly Thr His Gly Ser Leu Lys Thr Ser Ala Met Arg		
	1125	1130	1135
	Ser Asn Thr Arg Tyr Tyr Thr Gly Thr Gln Ser Arg Ile Arg Arg Met		
	1140	1145	1150
20	Trp Asn Asp Thr Val Arg Lys Gln Thr Glu Ser Ser Phe Met Ala Gly		
	1155	1160	1165
	Asp Ile Asn Ser Thr Pro Thr Leu Asn Arg Gly Thr Met Gly Asn His		
	1170	1175	1180
	Leu Leu Thr Asn Pro Val Leu Gln Pro Arg Gly Gly Thr Ser Pro Tyr		
25	1185	1190	1195
	1200		

09744226.012201

	Asn Thr Leu Ile Ala Glu Ser Val Gly Phe Asn Pro Ser Ser Pro Pro	
	1205	1210 1215
	Val Phe Asn Ser Pro Gly Ser Tyr Arg Glu Pro Lys His Pro Leu Gly	
	1220	1225 1230
5	Gly Arg Glu Ala Cys Gly Met Asp Thr Leu Pro Leu Asn Gly Asn Phe	
	1235	1240 1245
	Asn Asn Ser Tyr Ser Leu Arg Ser Gly Asp Phe Pro Pro Gly Asp Gly	
	1250	1255 1260
	Gly Pro Glu Pro Pro Arg Gly Arg Asn Leu Ala Asp Ala Ala Ala Phe	
10	1265	1270 1275 1280
	Glu Lys Met Ile Ile Ser Glu Leu Val His Asn Asn Leu Arg Gly Ser	
	1285	1290 1295
	Ser Ser Ala Ala Lys Gly Pro Pro Pro Pro Glu Pro Pro Val Pro Pro	
	1300	1305 1310
15	Val Pro Gly Gly Gly Gly Glu Glu Glu Ala Gly Gly Pro Gly Gly Ala	
	1315	1320 1325
	Asp Arg Ala Glu Ile Glu Leu Leu Tyr Lys Ala Leu Glu Glu Pro Leu	
	1330	1335 1340
	Leu Leu Pro Arg Ala Gln Ser Val Leu Tyr Gln Ser Asp Leu Asp Glu	
20	1345	1350 1355 1360
	Ser Glu Ser Cys Thr Ala Glu Asp Gly Ala Thr Ser Arg Pro Leu Ser	
	1365	1370 1375
	Ser Pro Pro Gly Arg Asp Ser Leu Tyr Ala Ser Gly Ala Asn Leu Arg	
	1380	1385 1390
25	Asp Ser Pro Ser Tyr Pro Asp Ser Ser Pro Glu Gly Pro Ser Glu Ala	

0974426-01201

1395 1400 1405
Leu Pro Pro Pro Pro Pro Ala Pro Pro Gly Pro Pro Glu Ile Tyr Tyr
1410 1415 1420
Thr Ser Arg Pro Pro Ala Leu Val Ala Arg Asn Pro Leu Gln Gly Tyr
5 1425 1430 1435 1440
Tyr Gln Val Arg Arg Pro Ser His Glu Gly Tyr Leu Ala Ala Pro Gly
1445 1450 1455
Leu Glu Gly Pro Gly Pro Asp Gly Asp Gly Gln Met Gln Leu Val Thr
1460 1465 1470
10 Ser Leu
<210> 6
<211> 4422
<212> DNA
<213> Human
15 <400> 6
ATGGCCCGCC TAGCCGCAGT GCTCTGGAAT CTGTGTGTCA CCGCCGTCCT GGTCACCTCG 60
GCCACCCAAG GCCTGAGCCG GGCCGGGCTC CCGTTCGGGC TGATGCGCCG GGAGCTGGCG 120
TGTGAAGGCT ACCCCATCGA GCTGCGGTGC CCCGGCAGCG ACGTCATCAT GGTGGAGAAT 180
GCCAACTACG GGCGCACGGA CGACAAGATT TGCGATGCTG ACCCTTTCCA GATGGAGAAT 240
20 GTGCAGTGCT ACCTGCCGGA CGCCTTCAAG ATCATGTCAC AGAGGTGTAA CAACCGCACC 300
CAGTGCGTGG TGGTCGCCGG CTCGGATGCC TTCCTGACC CCTGTCCTGG GACCTACAAG 360
TACCTGGAGG TGCAGTACGA CTGTGTCCCC TACAAAGTGG AGCAGAAAGT CTTCGTGTGC 420
CCAGGGACCC TGCAGAAGGT GCTGGAGCCC ACCTCGACAC ACGAGTCAGA GCACCACTCT 480
GGCGCATGGT GCAAGGACCC GCTGCAGGCG GGTGACCGCA TCTACGTGAT GCCCTGGATC 540
25 CCCTACCGCA CGGACACACT GACTGAGTAT GCCTCGTGGG AGGACTACGT GGCCGCCCGC 600

CACACCACCA CCTACCGCCT GCCCAACCGC GTGGATGGCA CAGGCTTTGT GGTCTACGAT 660
 GGTGCCGTCT TCTACAACAA GGAGCGCACG CGCAACATCG TCAAGTATGA CCTACGGACG 720
 CGCATCAAGA GCGGGGAGAC GGTCAATCAAT ACCGCCAACT ACCATGACAC CTCGCCCTAC 780
 CGCTGGGGCG GAAAGACCGA CATTGACCTG GCGGTGGACG AGAACGGGCT GTGGGTCATC 840
 5 TACGCCACTG AGGGCAACAA CGGGCGGCTG GTGGTGAGCC AGCTGAACCC CTACACACTG 900
 CGCTTTGAGG GCACGTGGGA GACGGGTAC GACAAGCGCT CGGCATCCAA CGCCTTCATG 960
 GTGTGTGGGG TCCTGTACGT CCTGCGCTCC GTGTACGTGG ATGATGACAG CGAGGCGGCT 1020
 GGCAACCGCG TGGACTATGC CTTCAACACC AATGCCAACC GCGAGGAGCC TGTACGCCTC 1080
 ACCTTCCCCA ACCCTACCA GTTCATCTCC TCCGTTGACT ACAACCCTCG CGACAACCAG 1140
 10 CTGTACGTCT GGAACAACCTA TTTCGTGGTG CGCTACAGCC TGGAGTTCGG GCCGCCCCGAC 1200
 CCCAGTGCTG GCCCAGCCAC TTCCCACCC CTCAGCACGA CCACCACAGC CAGGCCCCAG 1260
 CCCCTACCA GCACAGCCTC GCCCGCAGCC ACCACCCCGC TCCGCCGGGC ACCCCTCACC 1320
 ACGCACCCAG TGGGTGCCAT CAACCAGCTG GGACCTGATC TGCCTCCAGC CACAGCCCCA 1380
 GTCCCCAGCA CCCGGCGGCC CCCAGCCCCG AATCTACAG TGTCCCCTGA GCTCTTCTGC 1440
 15 GAGCCCCGAG AGGTACGGCG GGTCCAGTGG CCGGCCACCC AGCAGGGCAT GCTGGTGGAG 1500
 AGGCCCTGCC CCAAGGGGAC TCGAGGAATT GCCTCCTTCC AGTGTCTACC AGCCTTGGGG 1560
 CTCTGGAACC CCCGGGGCCC TGACCTCAGC AACTGCACCT CCCCTGGGT CAACCAGGTG 1620
 GCCCAGAAGA TCAAGAGTGG GGAGAACGCG GCCAACATCG CCAGCGAGCT GGCCCGACAC 1680
 ACCCGGGGCT CCATCTACGC GGGGGACGTC TCCTCCTCTG TGAAGCTGAT GGAGCAGCTG 1740
 20 CTGGACATCC TGGATGCCCC GCTGCAGGCC CTGCGGCCCA TCGAGCGCGA GTCAGCCGGC 1800
 AAGAACTACA ACAAGATGCA CAAGCGAGAG AGAACTTGTA AGGATTATAT CAAGGCCGTG 1860
 GTGGAGACAG TGGACAATCT GCTCCGGCCA GAAGCTCTGG AGTCCTGGAA GGACATGAAT 1920
 GCCACGGAGC AGGTGCACAC GGCCACCATG CTCCTCGACG TCCTGGAGGA GGGCGCCTTC 1980
 CTGCTGGCCG ACAATGTCAG GGAGCCTGCC CGCTTCCTGG CTGCCAAGGA GAACGTGGTC 2040
 25 CTGGAGGTCA CAGTCCTGAA CACAGAGGGC CAGGTGCAGG AGCTGGTGTT CCCCAGGAG 2100

GAGTACCCGA GAAAGAACTC CATCCAGCTG TCTGCCAAAA CCATCAAGCA GAACAGCCGC 2160
 AATGGGGTGG TCAAAGTTGT CTTATCCTC TACAACAACC TGGGCCTCTT CCTGTCCACG 2220
 GAGAATGCCA CAGTGAAGCT GGCCGGCGAA GCAGGCCCGG GTGGCCCTGG GGGCGCTCT 2280
 CTAGTGGTGA ACTCACAGGT CATCGCAGCA TCCATCAACA AGGAGTCCAG CCGCGTCTTC 2340
 5 CTCATGGACC CTGTCATCTT CACCGTGGCC CACCTGGAGG ACAAGAACCA CTTCAATGCT 2400
 AACTGCTCCT TCTGGAATA CTCGGAGCGT TCCATGCTGG GCTATTGGTC GACCCAAGGC 2460
 TGCCGCCTGG TGGAGTCCAA CAAGACCCAT ACCACGTGTG CCTGCAGCCA CCTCACCAAC 2520
 TTCGCTGTGC TCATGGCTCA CCGTGAGATC TACCAGGGCC GCATCAACGA GCTGCTGCTG 2580
 TCGGTCATCA CCTGGGTGGG CATTGTGATC TCCCTGGTCT GCTTGGCCAT CTGCATCTCC 2640
 10 ACCTTCTGCT TCCTGCGGGG GCTGCAGACC GACCGCAACA CCATCCACAA GAACCTGTGC 2700
 ATCAACCTCT TCCTGGCTGA GCTGCTCTTC CTGGTCGGGA TCGACAAGAC TCAGTATGAG 2760
 ATTGCCTGCC CCATCTTCGC CGGCCTGCTG CACTATTTCT TCCTGGCTGC CTTCTCCTGG 2820
 CTGTGCCTGG AGGGCGTGCA CCTCTACCTG CTACTAGTGG AGGTGTTTGA GAGCGAGTAT 2880
 TCCCGCACCA AGTACTACTA CCTGGGTGGC TACTGCTTCC CGGCCCTGGT GGTGGGCATC 2940
 15 GCGGCTGCCA TTGACTACCG CAGCTACGGC ACCGAGAAGG CCTGCTGGCT CCGAGTGGAC 3000
 AATTACTTCA TCTGGAGTTT CATCGGGCCA GTCTCCTTCG TTATCGTGGT CAACCTGGTG 3060
 TTCCTCATGG TGACCCTGCA CAAGATGATC CGAAGCTCAT CTGTGCTCAA GCCCGACTCC 3120
 AGCCGCCTGG ACAACATTAA ATCCTGGGCG CTGGGGGCCA TCGCGCTGCT GTTCCTGCTG 3180
 GGCCTCACCT GGGCTTTCGG CCTCCTCTTC ATCAACAAGG AGTCGGTGGT CATGGCCTAT 3240
 20 CTCTTCACCA CCTTCAACGC CTTCCAGGGG GTCTTCATCT TCGTCTTTCA CTGCGCCTTA 3300
 CAGAAGAAGG TGCACAAGGA GTACAGCAAG TGCCTGCGTC ACTCCTACTG CTGCATCCGC 3360
 TCCCCACCCG GGGGCACTCA CGGATCCCTC AAGACCTCAG CCATGCGAAG CAACACCCGC 3420
 TACTACACAG GGACCCAGAG CCGAATTCGG AGGATGTGGA ATGACACTGT GAGGAAACAG 3480
 ACGGAGTCCT CCTTCATGGC GGGTGACATC AACAGCACCC CCACCCTGAA CCGAGGTACC 3540
 25 ATGGGGAACC ACCTGCTGAC CAACCCCGTG CTGCAGCCCC GTGGGGGCAC CAGTCCCTAC 3600

AACACCCTCA TCGCCGAGTC AGTGGGCTTC AATCCCTCCT CGCCCCCTGT CTTCAACTCC 3660
 CCAGGGAGCT ACCGGGAACC CAAGCACCCC TTGGGAGGCC GGAAGCCTG TGGCATGGAC 3720
 ACCCTGCCCC TGAACGGCAA CTTCAATAAC AGTTACTCCT TCGAAGTGG GGATTTCCCT 3780
 CCCGGGGATG GGGGCCCTGA GCCGCCCCGA GGCCGGAACC TAGCCGATGC GCGGGCCTTT 3840
 5 GAGAAGATGA TCATCTCAGA GCTGGTGCAC AACAACCTGC GGGGGAGCAG CAGCGCGGCC 3900
 AAGGGCCCTC CACCGCCTGA GCCCCCTGTG CCACCTGTGC CAGGGGGCGG GGGCGAGGAA 3960
 GAGGCGGGCG GGGCCGGGGG TGCTGACCGG GCCGAGATTG AACTTCTCTA TAAGGCCCTG 4020
 GAGGAGCCTC TGCTGCTGCC CCGGGCCCAG TCGGTGCTGT ACCAGAGCGA TCTGGACGAG 4080
 TCGGAGAGCT GCACGGCCGA GGACGGCGCC ACCAGCCGGC CCCTCTCCTC CCCTCCTGGC 4140
 10 CGGGACTCCC TCTATGCCAG CGGGGCCAAC CTGCGGGACT CACCCTCCTA CCCGGACAGC 4200
 AGCCCTGAGG GGCCAGTGA GGCCCTGCCC CCACCCCTC CCGCACCCCC CGGCCCCCCC 4260
 GAAATCTACT ACACCTCGCG CCCGCCAGCC CTGGTGGCCC GGAATCCCCT GCAGGGCTAC 4320
 TACCAGGTGC GGCCTCCTAG CCACGAGGGC TACCTGGCAG CCCAGGCCT TGAGGGGCCA 4380
 GGGCCCAGTG GGGACGGCA GATGCAGCTG GTCACCAGTC TC 4425

15

SEQUENCE LISTING

<110> Ohara, Osamu
 <110> Nagase, Takahiro
 <110> Nomura, Nobuo
 <110> Hinuma, Shuji
 <110> Fujii, Ryo
 <110> Kitahara, Osamu
 <110> Mogi, Shinichi
 <120> Novel G Protein Coupled Receptor Protein and Its Use
 <130> 2534USOP
 <140>
 <141>
 <150> PCT/JP99/03909
 <151> 1998-07-22
 <150> JP 10-207579
 <151> 1998-07-23
 <150> JP 10-225060
 <151> 1998-08-07
 <150> JP 10-284328
 <151> 1998-10-06
 <160> 6
 <170>

<210> 1
 <211> 872
 <212> PRT
 <213> Human
 <400> 1

Ala	Glu	Gln	Thr	Arg	Asn	His	Leu	Asn	Ala	Gly	Asp	Ile	Thr	Tyr	Ser
1				5					10					15	
Val	Arg	Ala	Met	Asp	Gln	Leu	Val	Gly	Leu	Leu	Asp	Val	Gln	Leu	Arg
		20						25				30			
Asn	Leu	Thr	Pro	Gly	Gly	Lys	Asp	Ser	Ala	Ala	Arg	Ser	Leu	Asn	Lys
		35					40				45				
Ala	Met	Val	Glu	Thr	Val	Asn	Asn	Leu	Leu	Gln	Pro	Gln	Ala	Leu	Asn
	50					55				60					
Ala	Trp	Arg	Asp	Leu	Thr	Thr	Ser	Asp	Gln	Leu	Arg	Ala	Ala	Thr	Met
	65				70				75					80	
Leu	Leu	His	Thr	Val	Glu	Glu	Ser	Ala	Phe	Val	Leu	Ala	Asp	Asn	Leu
				85					90					95	
Leu	Lys	Thr	Asp	Ile	Val	Arg	Glu	Asn	Thr	Asp	Asn	Ile	Lys	Leu	Glu
			100					105				110			
Val	Ala	Arg	Leu	Ser	Thr	Glu	Gly	Asn	Leu	Glu	Asp	Leu	Lys	Phe	Pro
		115					120					125			
Glu	Asn	Met	Gly	His	Gly	Ser	Thr	Ile	Gln	Leu	Ser	Ala	Asn	Thr	Leu
	130					135					140				
Lys	Gln	Asn	Gly	Arg	Asn	Gly	Glu	Ile	Arg	Val	Ala	Phe	Val	Leu	Tyr
	145				150				155					160	
Asn	Asn	Leu	Gly	Pro	Tyr	Leu	Ser	Thr	Glu	Asn	Ala	Ser	Met	Lys	Leu
			165						170					175	
Gly	Thr	Glu	Ala	Leu	Ser	Thr	Asn	His	Ser	Val	Ile	Val	Asn	Ser	Pro
			180					185					190		
Val	Ile	Thr	Ala	Ala	Ile	Asn	Lys	Glu	Phe	Ser	Asn	Lys	Val	Tyr	Leu
		195					200					205			
Ala	Asp	Pro	Val	Val	Phe	Thr	Val	Lys	His	Ile	Lys	Gln	Ser	Glu	Glu
	210					215					220				
Asn	Phe	Asn	Pro	Asn	Cys	Ser	Phe	Trp	Ser	Tyr	Ser	Lys	Arg	Thr	Met
	225				230					235				240	
Thr	Gly	Tyr	Trp	Ser	Thr	Gln	Gly	Cys	Arg	Leu	Leu	Thr	Thr	Asn	Lys
			245						250					255	
Thr	His	Thr	Thr	Cys	Ser	Cys	Asn	His	Leu	Thr	Asn	Phe	Ala	Val	Leu
			260					265					270		
Met	Ala	His	Val	Glu	Val	Lys	His	Ser	Asp	Ala	Val	His	Asp	Leu	Leu
		275					280					285			
Leu	Asp	Val	Ile	Thr	Trp	Val	Gly	Ile	Leu	Leu	Ser	Leu	Val	Cys	Leu

290	295	300
Leu Ile Cys Ile Phe Thr	Phe Cys Phe Phe Arg	Gly Leu Gln Ser Asp
305	310	315
Arg Asn Thr Ile His Lys	Asn Leu Cys Ile Ser	Leu Phe Val Ala Glu
	325	330
Leu Leu Phe Leu Ile Gly	Ile Asn Arg Thr Asp	Gln Pro Ile Ala Cys
	340	345
Ala Val Phe Ala Ala Leu	Leu His Phe Phe Phe	Leu Ala Ala Phe Thr
	355	360
Trp Met Phe Leu Glu Gly	Val Gln Leu Tyr Ile Met	Leu Val Glu Val
	370	375
Phe Glu Ser Glu His Ser	Arg Arg Lys Tyr Phe	Tyr Leu Val Gly Tyr
	385	390
Gly Met Pro Ala Leu Ile	Val Ala Val Ser Ala	Ala Val Asp Tyr Arg
	405	410
Ser Tyr Gly Thr Asp Lys	Val Cys Trp Leu Arg	Leu Asp Thr Tyr Phe
	420	425
Ile Trp Ser Phe Ile Gly	Pro Ala Thr Leu Ile Ile	Met Leu Asn Val
	435	440
Ile Phe Leu Gly Ile Ala	Leu Tyr Lys Met Phe	His His Thr Ala Ile
	450	455
Leu Lys Pro Glu Ser Gly	Cys Leu Asp Asn Ile Lys	Ser Trp Val Ile
	465	470
Gly Ala Ile Ala Leu Leu	Cys Leu Leu Gly Leu	Thr Trp Ala Phe Gly
	485	490
Leu Met Tyr Ile Asn Glu	Ser Thr Val Ile Met	Ala Tyr Leu Phe Thr
	500	505
Ile Phe Asn Ser Leu Gln	Gly Met Phe Ile Phe Ile	Phe His Cys Val
	515	520
Leu Gln Lys Lys Val Arg	Lys Glu Tyr Gly Lys Cys	Leu Arg Thr His
	530	535
Cys Cys Ser Gly Lys Ser	Thr Glu Ser Ser Ile Gly	Ser Gly Lys Thr
	545	550
Ser Gly Ser Arg Thr Pro	Gly Arg Tyr Ser Thr	Gly Ser Gln Ser Arg
	565	570
Ile Arg Arg Met Trp Asn	Asp Thr Val Arg Lys Gln	Ser Glu Ser Ser
	580	585
Phe Ile Thr Gly Asp Ile	Asn Ser Ser Ala Ser	Leu Asn Arg Glu Gly
	595	600
Leu Leu Asn Asn Ala Arg	Asp Thr Ser Val Met	Asp Thr Leu Pro Leu
	610	615
Asn Gly Asn His Gly Asn	Ser Tyr Ser Ile Ala	Ser Gly Glu Tyr Leu
	625	630
Ser Asn Cys Val Gln Ile	Ile Asp Arg Gly Tyr	Asn His Asn Glu Thr
	645	650
Ala Leu Glu Lys Lys Ile	Leu Lys Glu Leu Thr	Ser Asn Tyr Ile Pro
	660	665
Ser Tyr Leu Asn Asn His	Glu Arg Ser Ser Glu	Gln Asn Arg Asn Leu
	675	680
Met Asn Lys Leu Val Asn	Asn Leu Gly Ser Gly	Arg Glu Asp Asp Ala
	690	695
Ile Val Leu Asp Asp Ala	Thr Ser Phe Asn His	Glu Glu Ser Leu Gly
	705	710
Leu Glu Leu Ile His Glu	Glu Glu Ser Asp Ala	Pro Leu Leu Pro Pro
	725	730
Val Tyr Ser Thr Glu Asn	His Gln Pro His His	Tyr Thr Arg Arg Arg
	740	745
Ile Pro Gln Asp His Ser	Glu Ser Phe Phe Pro	Leu Leu Thr Asn Glu
	755	760
His Thr Glu Asp Leu Gln	Ser Pro His Arg Asp	Ser Leu Tyr Thr Ser
	770	775
Met Pro Thr Leu Ala Gly	Val Ala Ala Thr Glu	Ser Val Thr Thr Ser
	785	790
Thr Gln Thr Glu Pro Pro	Pro Ala Lys Cys Gly	Asp Ala Glu Asp Val
	805	810
Tyr Tyr Lys Ser Met Pro	Asn Leu Gly Ser Arg	Asn His Val His Gln
	820	825
		830

Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
 835 840 845
 Val Pro Pro Asn Lys Asp Gly Thr Pro Pro Glu Gly Ser Ser Lys Gly
 850 855 860
 Pro Ala His Leu Val Thr Ser Leu
 865 870

<210> 2
 <211> 2616
 <212> DNA
 <213> Human
 <400> 2

GCTGAACAGA CAAGAAATCA CTTGAATGCT GGGGACATCA CCTACTCTGT CCGGGCCATG 60
 GACCAGCTGG TAGGCCCTCCT AGATGTACAG CTTTCGGAACCT TGACCCCAGG TGGAAAAGAT 120
 AGTGCTGCCC GGAGTTTGAA CAAGGCAATG GTCGAGACAG TTAACAACCT CCTTCAGCCA 180
 CAAGCTTTTGA ATGCATGGAG AGACCTGACT ACGAGTGATC AGCTGCGTGC GGCCACCATG 240
 TTGCTTCATA CTGTGGAGGA AAGTGCTTTT GTGCTGGCTG ATAACCTTTT GAAGACTGAC 300
 ATTGTTCAGGG AGAATACAGA CAATATTAAA TTGGAAGTTG CAAGACTGAG CACAGAAGGA 360
 AACTTAGAAG ACCTAAAATT TCCAGAAAAC ATGGGCCATG GAAGCACTAT CCAGCTGTCT 420
 GCAAATACCT TAAAGCAAAA TGGCCGAAAT GGAGAGATCA GAGTGGCCTT TGTCTGTAT 480
 AACAACTTGG GTCCCTTATTT ATCCACGGAG AATGCCAGTA TGAAGTTGGG AACCGAAGCT 540
 TTGTCCACAA ATCATTTCTGT TATTGTCAAT TCCCCTGTTA TTACGGCAGC AATAAACAAA 600
 GAGTTCAGTA ACAAGGTTTA TTTGGCTGAT CCTGTGGTAT TTAAGTTTAA ACATATCAAG 660
 CAGTCAGAGG AAAATTTTCAA CCCTAACTGT TCATTTTGGG GCTACTCCAA GCGTACAATG 720
 ACAGGTTATT GGTCAACACA AGGCTGTCTG CTCCTGACAA CAAATAAGAC ACATACTACA 780
 TGCTCTTGTA ACCACCTAAC AAATTTTGCA GTACTGATGG CACATGTGGA AGTTAAGCAC 840
 AGTGATGCGG TCCATGACCT CCTTCTGGAT GTGATCACGT GGGTTGGAAT TTTGCTGTCC 900
 CTTGTTTGTC TCCTGATTTG CATCTTCACA TTTTGCTTTT TCCGCGGGCT CCAGAGTGAC 960
 CGTAACACCA TCCACAAGAA CCTCTGCATC AGTCTCTTTG TAGCAGAGCT GCTCTTCTCT 1020
 ATTGGGATCA ACCGAACTGA CCAACCAATT GCCTGTGCTG TTTTCGCTGC CCTGTTTCT 1080
 TCTTCTTGGC TGCCCTTCACC TGGATGTTCC TGGAGGGGGT GCAGCTTTAT ATACATCATG 1140
 CTGGTGGAGG TTTTGTGAGG TGAACATTCA CGTAGGAAAT ACTTTTATCT GGTGCGCTAT 1200
 GGGATGCCTG CACTCATTTG GGCTGTGTCA GCTGCAGTAG ACTACAGGAG TTATGGAACA 1260
 GATAAAGTAT GTTGGCTCCG ACTTGACACC TACTTCAATT GGAGTTTAT AGGACCAGCA 1320
 ACTTTGATAA TTATGCTTAA TGAATCTTC CTTGGGATTG CTTTATATAA AATGTTTCAT 1380
 CATACTGCTA TACTGAAACC TGAATCAGGC TGTCTTGATA ACATCAAGTC ATGGGTATATA 1440
 GGTGCAATAG CTCTTCTCTG CCTATTAGGA TTGACCTGGG CCTTTGGAAT CATGTATATT 1500
 AATGAAAGCA CAGTCATCAT GGCTTATCTC TTCACCATT TCAATTCCTT ACAGGGGAATG 1560
 TTTATATTTA TTTTCCATTG TGTCTACAG AAGAAGGTAC GAAAAGAGTA TGGGAAATGC 1620
 CTGCGAACAC ATTGCTGTAG TGGCAAAAGT ACAGAGAGTT CCATTGGTTC AGGGAAAACA 1680
 TCTGGTTCTC GAACTCCTGG ACAGTACTCC ACAGGCTCAC AGAGCCGAAT CCGTAGAATG 1740
 TGGAATGACA CGGTTGCAAA GCAGTCAGAG TCTTCCTTTA TTAAGGAGA CATAAACAGT 1800
 TCAGCGTCAC TCAACAGAGA GGGGCTTCTG AACAATGCCA GGGATACAAG TGTATGATG 1860
 ACTCTACCAC TGAATGGTAA CCATGGCAAT AGTTACAGCA TTGCCAGCGG CGAATACCTG 1920
 AGCAACTGTG TGCAAAATCAT AGACCGTGGC TATAACCATA ACGAGACCGC CCTAGAGAAA 1980
 AAGATTCTGA AGGAACTCAC TTCCAATAT ATCCCTTCTT ACCTGAACAA CCATGAGCGC 2040
 TCCAGTGAAC AGAACAGGAA TCTGATGAAC AAGCTGGTGA ATAACCTTGG CAGTGAAGG 2100
 GAAGATGATG CCATTGTCTT GGATGATGCC ACCTCGTTTA ACCACGAGGA GAGTTTGGGC 2160
 CTGGAATCA TTTATGAGGA ATCTGATGCT CTTTGTCTGC CCCCAAGAGT ATACTCCACC 2220
 GAGAACCACC AGCCACACCA TTATACCAGA AGGCGGATCC CCCAAGACCA CAGTGAGAGC 2280
 TTTTTCCTTT TGCTAACCAA CGAGCACACA GAAGATCTCC AGTCACCCCA TAGAGACTCT 2340
 CTCTATACCA GCATGCCGAC ACTGGCTGGT GTGGCCGCCA CAGAGAGTGT TACCACCAGC 2400
 ACCCAGACCG AACCCCAACC GGCCAAATGT GGTGATGCCG AAGATGTTTA CTACAAAAGC 2460
 ATGCCAAACC TAGGCTCCAG AAACCACGTC CATCAGCTGC ATACTTACTA CCAGCTAGGT 2520
 CGCGGCAGCA GTGATGGATT TATAGTTTCT CCAAACAAAG ATGGGACCCC TCCCAGGGA 2580
 AGTTCAAAAG GACCGGCTCA TTTGGTCACT AGTCTA 2616

<210> 3
 <211> 1021
 <212> PRT
 <213> Human
 <400> 3

Glu Gly Ser Lys Gly Thr Lys Pro Pro Pro Ala Val Ser Thr Thr Lys
 1 5 10 15
 Ile Pro Pro Ile Thr Asn Ile Phe Pro Leu Pro Glu Arg Phe Cys Glu

[illegible]

Thr	Phe	Ile	Ile	Leu	Leu	Asn	Ile	Ile	Phe	Leu	Val	Ile	Thr	Leu	Cys
Lys	Met	Val	Lys	His	Ser	Asn	Thr	Leu	Lys	Pro	Asp	Ser	Ser	Arg	Leu
Glu	Asn	Ile	Lys	Ser	Trp	Val	Leu	Gly	Ala	Phe	Ala	Leu	Leu	Cys	Leu
Leu	Gly	Leu	Thr	Trp	Ser	Phe	Gly	Leu	Leu	Phe	Ile	Asn	Glu	Glu	Thr
Ile	Val	Met	Ala	Tyr	Leu	Phe	Thr	Ile	Phe	Asn	Ala	Phe	Gln	Gly	Val
Phe	Ile	Phe	Ile	Phe	His	Cys	Ala	Leu	Gln	Lys	Lys	Val	Arg	Lys	Glu
Tyr	Gly	Lys	Cys	Phe	Arg	His	Ser	Tyr	Cys	Cys	Gly	Gly	Leu	Pro	Thr
Glu	Ser	Pro	His	Ser	Ser	Val	Lys	Ala	Ser	Thr	Thr	Arg	Thr	Ser	Ala
Arg	Tyr	Ser	Ser	Gly	Thr	Gln	Ser	Arg	Ile	Arg	Arg	Met	Trp	Asn	Asp
Thr	Val	Arg	Lys	Gln	Ser	Glu	Ser	Ser	Phe	Ile	Ser	Gly	Asp	Ile	Asn
Ser	Thr	Ser	Thr	Leu	Asn	Gln	Gly	Met	Thr	Gly	Asn	Tyr	Leu	Leu	Thr
Asn	Pro	Leu	Leu	Arg	Pro	His	Gly	Thr	Asn	Asn	Pro	Tyr	Asn	Thr	Leu
Leu	Ala	Glu	Thr	Val	Val	Cys	Asn	Ala	Pro	Ser	Ala	Pro	Val	Phe	Asn
Ser	Pro	Gly	His	Ser	Leu	Asn	Asn	Ala	Arg	Asp	Thr	Ser	Ala	Met	Asp
Thr	Leu	Pro	Leu	Asn	Gly	Asn	Phe	Asn	Asn	Ser	Tyr	Ser	Leu	His	Lys
Gly	Asp	Tyr	Asn	Asp	Ser	Val	Gln	Val	Val	Asp	Cys	Gly	Leu	Ser	Leu
Asn	Asp	Thr	Ala	Phe	Glu	Lys	Met	Ile	Ile	Ser	Glu	Leu	Val	His	Asn
Asn	Leu	Arg	Gly	Ser	Ser	Lys	Thr	His	Asn	Leu	Glu	Leu	Thr	Leu	Pro
Val	Lys	Pro	Val	Ile	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	Ala	Ile	Val
Ala	Asp	Ala	Ser	Ser	Leu	Met	His	Ser	Asp	Asn	Pro	Gly	Leu	Glu	Leu
His	His	Lys	Glu	Leu	Glu	Ala	Pro	Leu	Ile	Pro	Gln	Arg	Thr	His	Ser
Leu	Leu	Tyr	Gln	Pro	Gln	Lys	Lys	Val	Lys	Ser	Glu	Gly	Thr	Asp	Ser
Tyr	Val	Ser	Gln	Leu	Thr	Ala	Glu	Ala	Glu	Asp	His	Leu	Gln	Ser	Pro
Asn	Arg	Asp	Ser	Leu	Tyr	Thr	Ser	Met	Pro	Asn	Leu	Arg	Asp	Ser	Pro
Tyr	Pro	Glu	Ser	Ser	Pro	Asp	Met	Glu	Glu	Asp	Leu	Ser	Pro	Ser	Arg
Arg	Ser	Glu	Asn	Glu	Asp	Ile	Tyr	Tyr	Lys	Ser	Met	Pro	Asn	Leu	Gly
Ala	Gly	His	Gln	Leu	Gln	Met	Cys	Tyr	Gln	Ile	Ser	Arg	Gly	Asn	Ser
Asp	Gly	Tyr	Ile	Ile	Pro	Ile	Asn	Lys	Glu	Gly	Cys	Ile	Pro	Glu	Gly
Asp	Val	Arg	Glu	Gly	Gln	Met	Gln	Leu	Val	Thr	Ser	Leu			

<210>	4
<211>	3063
<212>	DNA
<213>	Human
<400>	4

Page 5

09744225-012201

TGGCCTCAGA	CACAAAGGGG	AATGATGGTT	GAACGACCAT	GCCCTAAGGG	AACAAGAGGA	180
ACTGCCTCAT	ATCTCTGCAT	GATTTCCACT	GGAACATGGA	ACCCTAAGGG	CCCCGATCTT	240
AGCAACTGTA	CCTCACACTG	GGTGAATCAG	CTGGCTCAGA	AGATCAGAAG	CGGAGAAAAT	300
GCTGCTAGTC	TTGCCAATGA	ACTGGCTAAA	CATACCAAAG	GGCCAGTGT	TGCTGGGGAT	360
GTAAGTTCCT	CAGTGAGATT	GATGGAGCAG	TTGGTGGACA	TCCTTGATGC	ACAGCTGCAG	420
GAAGTGAAC	CTAGTGAATA	AGATTTCAGCT	GGACGGAGTT	ATAACAAGCT	CCAAAAACGA	480
GAGAAGACAT	GCAGGGCTTA	CCTTAAGGCA	ATTGTTGACA	CAGTGGACAA	CCTTCTGAGA	540
CCTGAAGCTT	TGGAATCATG	GAAACATATG	AATTCTTCTG	AACAAGCACA	TACTGCAACA	600
ATGTTACTCG	ATACATTGGA	AGAAGGAGCT	TTTGTCTTAG	CTGACAATCT	TTTAGAACCA	660
ACAAGGGTCT	CAATGCCAC	AGAAAATATT	GTCCTGGAAG	TTGCCGTACT	CAGTACAGAA	720
GGACAGATCC	AAGACTTTAA	ATTTCTCTG	GGCATCAAAG	GAGCAGGCAG	CTCAATCCAA	780
CTGTCCGCAA	ATACCGTCAA	ACAGAACAGC	AGGAATGGGC	TTGCAAAGTT	GGTGTTCATC	840
ATTTACCGGA	GCCTGGGACA	GTTCTTAGT	ACAGAAAATG	CAACCAATTAA	ACTGGGTGCT	900
GATTTTATTG	GTCGTAATAG	CACCATTGCA	GTGAACTCTC	ACGTCAATTC	AGTTTCAATC	960
AATAAAGAGT	CCAGCCGAGT	ATACCTGACT	GATCCTGTGC	TTTTTACCCT	GCCACACATT	1020
GATCCTGACA	ATTATTTCAA	TGCAAACTGC	TCCTTCTGGA	ACTACTCAGA	GAGAACTATG	1080
ATGGGATATT	GGTCTACCCA	GGGCTGCAAG	CTGGTTGACA	CTAATAAAAC	TCGAACAACG	1140
TGTGCATGCA	GCCACCTAAC	CAATTTTGCA	ATTCTCATGG	CCCACAGGGA	AATTCGATAT	1200
AAAGATGGCG	TTCATGAATT	ACTTCTTACA	GTCATCACCT	GGGTGGGAAT	TGTCATTTCC	1260
CTTGTTTTGCC	TGGCTATCTG	CATCTTCACC	TTCTGCTTTT	TCCGTGGCCT	ACAGAGTGAC	1320
CGAAATACTA	TTCACAAGAA	CCTTTGTATC	AACCTTTTCA	TTGCTGAATT	TATTTTCCCTA	1380
ATAGGCATTG	ATAAGACAAA	ATATGCGATT	GATGCCCCAA	TATTTGCAGG	ACTTCTACAC	1440
TTTTTCTTTT	TGGCAGCTTT	TGCTTGGATG	TGCCTAGAAG	GTGTGCAGCT	CTACCTAATG	1500
TTAGTTGAAG	TTTTTGAAG	TGAATATTCA	AGGAAAAAAT	ATTACTATGT	TGCTGGTTAC	1560
TTGTTTCCTG	CCACAGTGGT	TGGAGTTTCA	GCTGCTATTG	ACTATAAGAG	CTATGGAACA	1620
GAAAAAGCTT	GCTGGCTTCA	TGTTGATAAC	TACTTTTATAT	GGAGCTTCAT	TGGACCTGTT	1680
ACCTTCATTA	TTCTGTGTA	TATTATCTTC	TTGGTGATCA	CATTGTGCAA	AATGGTGAAG	1740
CATTCAAACA	CTTTGAAACC	AGATTCTAGC	AGGTTGGAAA	ACATTAAGTC	TTGGGTGCTT	1800
GGCGCTTTTC	CTCTTCTGTG	TCTTCTTGGC	CTCACCTGGT	CCTTTGGGTT	GCTTTTATT	1860
AATGAGGAGA	CTATTGTGAT	GGCATATCTC	TTCACTATAT	TTAATGCTTT	CCAGGGAGTG	1920
TTCAATTTTCA	TCTTTCACTG	TGCTCTCCAA	AAGAAAGTAC	GAAAAGAATA	TGGCAAGTGC	1980
TTCAGACACT	CATACTGCTG	TGGAGGCCCT	CCAACGTAGA	GTCCCCACAG	TTCACTGAAG	2040
GCATCAACCA	CCAGAACCAG	TGCTCGCTAT	TCCTCTGGCA	CACAGAGTCG	TATAAGAAGA	2100
ATGTGGAATG	ATACTGTGAG	AAAACAATCA	GAATCTTCTT	TTATCTCAGG	TGACATCAAT	2160
AGCACTTCAA	CACTTAATCA	AGGAATGACT	GGCAATTACC	TACTAACAAA	CCCTCTCTTT	2220
CGACCCACG	GCACTAACAA	CCCCTATAAC	ACATTGCTCG	CTGAAACAGT	TGTATGTAAT	2280
CCCCCTTCAG	CTCCTGTATT	TAACCTACCA	GGACATTAC	TGAACAATGC	CAGGGATACA	2340
AGTGCCATGG	ATACTCTACC	GCTAAATGGT	AATTTTAACA	ACAGCTACTC	GCTGCACAAG	2400
GGTGAATATA	ATGACAGCGT	GCAAGTTGTG	GACTGTGGAC	TAAGTCTGAA	TGATACTGCT	2460
TTTGAGAAAA	TGATCATTTT	AGAATTAGTG	CACAACAAC	TACGGGGCAG	CAGCAAGACT	2520
CACAACCTCG	AGCTACGCTG	ACCAGTCAAA	CCTGTGATTG	GAGGTAGCAG	CAGTGAAGAT	2580
GATGCTATTG	TGGCAGATGC	TTTCATCTTTA	ATGCACAGCG	ACAACCCAGG	GCTGGAGCTC	2640
CATCACAAG	AACCTCGAGG	ACCACTTATT	CCTCAGCGGA	CTCACTCCCT	TCTGTACCAA	2700
CCCCAGAAGA	AAGTGAAGTC	CGAGGGAAC	GACAGCTATG	TCTCCCAACT	GACAGCAGAG	2760
GCTGAAGATC	ACCTACAGTC	CCCCAACAGA	GACTCTCTTT	ATACAAGCAT	GCCCCAATCTT	2820
AGAGACTCTC	CCTATCCGGA	GAGCAGCCCT	GACATGGAAG	AAGACCTCTC	TCCCTCCAGG	2880
AGGAGTGAGA	ATGAGGACAT	TTACTATAAA	AGCATGCCAA	ATCTTGGAGC	TGGCCATCAG	2940
CTTCAGATGT	GCTACCAGAT	CAGCAGGGGC	AATAGTGATG	GTTATATAAT	CCCCATTAAC	3000
AAAGAAGGGT	GTATTCCAGA	AGGAGATGTT	AGAGAAGGAC	AAATGCAGCT	GGTTACAAG	3060
CTT						3063

<210> 5
 <211> 1474
 <212> PRT
 <213> Human
 <400> 5

Met	Ala	Arg	Leu	Ala	Ala	Val	Leu	Trp	Asn	Leu	Cys	Val	Thr	Ala	Val
			5					10						15	
Leu	Val	Thr	Ser	Ala	Thr	Gln	Gly	Leu	Ser	Arg	Ala	Gly	Leu	Pro	Phe
			20					25					30		
Gly	Leu	Met	Arg	Arg	Glu	Leu	Ala	Cys	Glu	Gly	Tyr	Pro	Ile	Glu	Leu
		35					40					45			
Arg	Cys	Pro	Gly	Ser	Asp	Val	Ile	Met	Val	Glu	Asn	Ala	Asn	Tyr	Gly
	50					55					60				
Arg	Thr	Asp	Asp	Lys	Ile	Cys	Asp	Ala	Asp	Pro	Phe	Gln	Met	Glu	Asn
	65				70				75					80	

09744226 "012201

Val	Gln	Cys	Tyr	Leu	Pro	Asp	Ala	Phe	Lys	Ile	Met	Ser	Gln	Arg	Cys	
				85					90					95		
Asn	Asn	Arg	Thr	Gln	Cys	Val	Val	Val	Ala	Gly	Ser	Asp	Ala	Phe	Pro	
			100						105				110			
Asp	Pro	Cys	Pro	Gly	Thr	Tyr	Lys	Tyr	Leu	Glu	Val	Gln	Tyr	Asp	Cys	
		115					120					125				
Val	Pro	Tyr	Lys	Val	Glu	Gln	Lys	Val	Phe	Val	Cys	Pro	Gly	Thr	Leu	
	130					135					140					
Gln	Lys	Val	Leu	Glu	Pro	Thr	Ser	Thr	His	Glu	Ser	Glu	His	Gln	Ser	
145					150					155					160	
Gly	Ala	Trp	Cys	Lys	Asp	Pro	Leu	Gln	Ala	Gly	Asp	Arg	Ile	Tyr	Val	
				165					170					175		
Met	Pro	Trp	Ile	Pro	Tyr	Arg	Thr	Asp	Thr	Leu	Thr	Glu	Tyr	Ala	Ser	
			180					185					190			
Trp	Glu	Asp	Tyr	Val	Ala	Ala	Arg	His	Thr	Thr	Thr	Tyr	Arg	Leu	Pro	
		195					200					205				
Asn	Arg	Val	Asp	Gly	Thr	Gly	Phe	Val	Val	Tyr	Asp	Gly	Ala	Val	Phe	
	210					215					220					
Tyr	Asn	Lys	Glu	Arg	Thr	Arg	Asn	Ile	Val	Lys	Tyr	Asp	Leu	Arg	Thr	
225					230					235					240	
Arg	Ile	Lys	Ser	Gly	Glu	Thr	Val	Ile	Asn	Thr	Ala	Asn	Tyr	His	Asp	
				245					250					255		
Thr	Ser	Pro	Tyr	Arg	Trp	Gly	Gly	Lys	Thr	Asp	Ile	Asp	Leu	Ala	Val	
			260				265						270			
Asp	Glu	Asn	Gly	Leu	Trp	Val	Ile	Tyr	Ala	Thr	Glu	Gly	Asn	Asn	Gly	
		275					280					285				
Arg	Leu	Val	Val	Ser	Gln	Leu	Asn	Pro	Tyr	Thr	Leu	Arg	Phe	Glu	Gly	
	290					295					300					
Thr	Trp	Glu	Thr	Gly	Tyr	Asp	Lys	Arg	Ser	Ala	Ser	Asn	Ala	Phe	Met	
305					310					315					320	
Val	Cys	Gly	Val	Leu	Tyr	Val	Leu	Arg	Ser	Val	Tyr	Val	Asp	Asp	Asp	
				325					330				335			
Ser	Glu	Ala	Ala	Gly	Asn	Arg	Val	Asp	Tyr	Ala	Phe	Asn	Thr	Asn	Ala	
			340					345					350			
Asn	Arg	Glu	Pro	Val	Ser	Leu	Thr	Phe	Pro	Asn	Pro	Tyr	Gln	Phe		
		355					360				365					
Ile	Ser	Ser	Val	Asp	Tyr	Asn	Pro	Arg	Asp	Asn	Gln	Leu	Tyr	Val	Trp	
	370					375					380					
Asn	Asn	Tyr	Phe	Val	Val	Arg	Tyr	Ser	Leu	Glu	Phe	Gly	Pro	Pro	Asp	
385					390					395					400	
Pro	Ser	Ala	Gly	Pro	Ala	Thr	Ser	Pro	Pro	Leu	Ser	Thr	Thr	Thr	Thr	
				405					410					415		
Ala	Arg	Pro	Thr	Pro	Leu	Thr	Ser	Thr	Ala	Ser	Pro	Ala	Ala	Thr	Thr	
			420					425					430			
Pro	Leu	Arg	Arg	Ala	Pro	Leu	Thr	His	Pro	Val	Gly	Ala	Ile	Asn		
		435					440				445					
Gln	Leu	Gly	Pro	Asp	Leu	Pro	Pro	Ala	Thr	Ala	Pro	Val	Pro	Ser	Thr	
	450					455				460						
Arg	Arg	Pro	Pro	Ala	Pro	Asn	Leu	His	Val	Ser	Pro	Glu	Leu	Phe	Cys	
465					470					475					480	
Glu	Pro	Arg	Glu	Val	Arg	Arg	Val	Gln	Trp	Pro	Ala	Thr	Gln	Gln	Gly	
				485					490					495		
Met	Leu	Val	Glu	Arg	Pro	Cys	Pro	Lys	Gly	Thr	Arg	Gly	Ile	Ala	Ser	
			500					505					510			
Phe	Gln	Cys	Leu	Pro	Ala	Leu	Gly	Leu	Trp	Asn	Pro	Arg	Gly	Pro	Asp	
		515					520					525				
Leu	Ser	Asn	Cys	Thr	Ser	Pro	Trp	Val	Asn	Gln	Val	Ala	Gln	Lys	Ile	
		530				535					540					
Lys	Ser	Gly	Glu	Asn	Ala	Ala	Asn	Ile	Ala	Ser	Glu	Leu	Ala	Arg	His	
545					550					555					560	
Thr	Arg	Gly	Ser	Ile	Tyr	Ala	Gly	Asp	Val	Ser	Ser	Ser	Val	Lys	Leu	
				565					570					575		
Met	Glu	Gln	Leu	Leu	Asp	Ile	Leu	Asp	Ala	Gln	Leu	Gln	Ala	Leu	Arg	
			580					585					590			
Pro	Ile	Glu	Arg	Glu	Ser	Ala	Gly	Lys	Asn	Tyr	Asn	Lys	Met	His	Lys	
		595					600					605				
Arg	Glu	Arg	Thr	Cys	Lys	Asp	Tyr	Ile	Lys	Ala	Val	Val	Glu	Thr	Val	

610	615	620			
Asp Asn Leu Leu Arg Pro	Glu Ala Leu Glu Ser	Trp Lys Asp Met Asn			
625	630	635			640
Ala Thr Glu Gln Val His	Thr Ala Thr Met Leu	Leu Leu Asp Val Leu			Glu
	645	650			655
Glu Gly Ala Phe Leu Leu	Ala Asp Asn Val Arg	Glu Pro Ala Arg Phe			
	660	665			670
Leu Ala Ala Lys Glu Asn	Val Val Leu Glu Val	Thr Val Leu Asn Thr			
	675	680			685
Glu Gly Gln Val Gln Glu	Leu Val Phe Pro Gln	Glu Glu Tyr Pro Arg			
	690	695			700
Lys Asn Ser Ile Gln Leu	Ser Ala Lys Thr Ile	Lys Gln Asn Ser Arg			
705	710	715			720
Asn Gly Val Val Lys Val	Val Phe Ile Leu Tyr	Asn Asn Leu Gly Leu			
	725	730			735
Phe Leu Ser Thr Glu Asn	Ala Thr Val Lys Leu	Ala Gly Glu Ala Gly			
	740	745			750
Pro Gly Gly Pro Gly Gly	Ala Ser Leu Val Val	Asn Ser Gln Val Ile			
	755	760			765
Ala Ala Ser Ile Asn Lys	Glu Ser Ser Arg Val	Phe Leu Met Asp Pro			
	770	775			780
Val Ile Phe Thr Val Ala	His Leu Glu Asp Lys	Asn His Phe Asn Ala			
785	790	795			800
Asn Cys Ser Phe Trp Asn	Tyr Ser Glu Arg Ser	Met Leu Gly Tyr Trp			
	805	810			815
Ser Thr Gln Gly Cys Arg	Leu Val Glu Ser Asn	Lys Thr His Thr Thr			
	820	825			830
Cys Ala Cys Ser His Leu	Thr Asn Phe Ala Val	Leu Met Ala His Arg			
	835	840			845
Glu Ile Tyr Gln Gly Arg	Ile Asn Glu Leu Leu	Leu Ser Val Ile Thr			
	850	855			860
Trp Val Gly Ile Val Ile	Ser Leu Val Cys Leu	Ala Ile Cys Ile Ser			
865	870	875			880
Thr Phe Cys Phe Leu Arg	Gly Leu Gln Thr Asp	Arg Asn Thr Ile His			
	885	890			895
Lys Asn Leu Cys Ile Asn	Leu Phe Leu Ala Glu	Leu Leu Phe Leu Val			
	900	905			910
Gly Ile Asp Lys Thr Gln	Tyr Glu Ile Ala Cys	Pro Ile Phe Ala Gly			
	915	920			925
Leu Leu His Tyr Phe Phe	Leu Ala Ala Phe Ser	Trp Leu Cys Leu Glu			
	930	935			940
Gly Val His Leu Tyr Leu	Leu Leu Leu Val Glu	Val Phe Glu Ser Glu			
945	950	955			960
Ser Arg Thr Lys Tyr Tyr	Tyr Tyr Leu Gly Gly	Tyr Cys Phe Pro Ala			
	965	970			975
Val Val Gly Ile Ala Ala	Ile Asp Tyr Arg Ser	Tyr Gly Thr Glu			
	980	985			990
Lys Ala Cys Trp Leu Arg	Val Asp Asn Tyr Phe	Ile Trp Ser Phe Ile			
	995	1000			1005
Gly Pro Val Ser Phe Val	Ile Val Val Asn Leu	Val Phe Leu Met Val			
	1010	1015			1020
Thr Leu His Lys Met Ile	Arg Ser Ser Ser Val	Leu Lys Pro Asp Ser			
1025	1030	1035			1040
Ser Arg Leu Asp Asn Ile	Lys Ser Trp Ala Leu	Gly Ala Ile Ala Leu			
	1045	1050			1055
Leu Phe Leu Leu Gly Leu	Thr Trp Ala Phe Gly	Leu Leu Phe Ile Asn			
	1060	1065			1070
Lys Glu Ser Val Val Met	Ala Tyr Leu Phe Thr	Thr Phe Asn Ala Phe			
	1075	1080			1085
Gln Gly Val Phe Ile Phe	Val Phe His Cys Ala	Leu Gln Lys Lys Val			
	1090	1095			1100
His Lys Glu Tyr Ser Lys	Cys Leu Arg His Ser	Tyr Cys Cys Ile Arg			
1105	1110	1115			1120
Ser Pro Pro Gly Gly Thr	His Gly Ser Leu Lys	Thr Ser Ala Met Arg			
	1125	1130			1135
Ser Asn Thr Arg Tyr Tyr	Thr Gly Thr Gln Ser	Arg Ile Arg Arg Met			
	1140	1145			1150

Trp Asn Asp Thr Val Arg Lys Gln Thr Glu Ser Ser Phe Met Ala Gly
 1155 1160 1165
 Asp Ile Asn Ser Thr Pro Thr Leu Asn Arg Gly Thr Met Gly Asn His
 1170 1175 1180
 Leu Leu Thr Asn Pro Val Leu Gln Pro Arg Gly Gly Thr Ser Pro Tyr
 1185 1190 1195 1200
 Asn Thr Leu Ile Ala Glu Ser Val Gly Phe Asn Pro Ser Ser Pro Pro
 1205 1210 1215
 Val Phe Asn Ser Pro Gly Ser Tyr Arg Glu Pro Lys His Pro Leu Gly
 1220 1225 1230
 Gly Arg Glu Ala Cys Gly Met Asp Thr Leu Pro Leu Asn Gly Asn Phe
 1235 1240 1245
 Asn Asn Ser Tyr Ser Leu Arg Ser Gly Asp Phe Pro Pro Gly Asp Gly
 1250 1255 1260
 Gly Pro Glu Pro Pro Arg Gly Arg Asn Leu Ala Asp Ala Ala Ala Phe
 1265 1270 1275 1280
 Glu Lys Met Ile Ile Ser Glu Leu Val His Asn Asn Leu Arg Gly Ser
 1285 1290 1295
 Ser Ser Ala Ala Lys Gly Pro Pro Pro Pro Glu Pro Pro Val Pro Pro
 1300 1305 1310
 Val Pro Gly Gly Gly Glu Glu Ala Gly Gly Pro Gly Gly Ala
 1315 1320 1325
 Asp Arg Ala Glu Ile Glu Leu Leu Tyr Lys Ala Leu Glu Glu Pro Leu
 1330 1335 1340
 Leu Leu Pro Arg Ala Gln Ser Val Leu Tyr Gln Ser Asp Leu Asp Glu
 1345 1350 1355 1360
 Ser Glu Ser Cys Thr Ala Glu Asp Gly Ala Thr Ser Arg Pro Leu Ser
 1365 1370 1375
 Ser Pro Pro Gly Arg Asp Ser Leu Tyr Ala Ser Gly Ala Asn Leu Arg
 1380 1385 1390
 Asp Ser Pro Ser Tyr Pro Asp Ser Ser Pro Glu Gly Pro Ser Glu Ala
 1395 1400 1405
 Leu Pro Pro Pro Pro Pro Ala Pro Pro Gly Pro Pro Glu Ile Tyr Tyr
 1410 1415 1420
 Thr Ser Arg Pro Pro Ala Leu Val Ala Arg Asn Pro Leu Gln Gly Tyr
 1425 1430 1435 1440
 Tyr Gln Val Arg Arg Pro Ser His Glu Gly Tyr Leu Ala Ala Pro Gly
 1445 1450 1455
 Leu Glu Gly Pro Gly Pro Asp Gly Asp Gly Gln Met Gln Leu Val Thr
 1460 1465 1470
 Ser Leu

<210> 6
 <211> 4422
 <212> DNA
 <213> Human
 <400> 6

ATGGCCCGCC TAGCCGCACT GCTCTGGAAT CTGTGTGTCA CCGCCGTCCT GGTCACCTCG 60
 GCCACCCAAG GCCTGAGCCG GGCCGGGCTC CCGTTCGGGC TGATGCGCCG GGAGCTGGCG 120
 TGTGAAGGCT ACCCCATCGA GCTGCGGTGC CCCGGCAGCG ACGTCATCAT GGTGGAGAAT 180
 GCCAACTACG GGCACACGGA CGACAAGATT TGCGATGCTG ACCCTTTCCA GATGGAGAAT 240
 GTGCAGTGCT ACCTGCCGGA CGCCTTCAAG ATCATGTACAC AGAGGTGTAA CAACCGCACC 300
 CAGTGCGTGG TGGTCGCCGG CTCGGATGCC TTTCTGACC CCTGTCTTGG GACCTACAAG 360
 TACCTGGAGG TGCAGTACGA CTGTGTCCCC TACAAAGTGG AGCAGAAAGT CTTCGTGTGC 420
 CCAGGGACCC TGCAGAAGGT GCTGGAGCCC ACCTCGACAC ACGAGTCAGA GCACCACTCT 480
 GGCGCATGGT GCAAGGACCC GCTGCAGGCG GGTGACCGCA TCTACGTGAT GCCCTGGATC 540
 CCCTACCGCA CGGACACACT GACTGAGTAT GCCTCGTGGG AGGACTACGT GGCCGCCCGC 600
 CACACCACCA CCTACCGCCT GCCCAACCGC GTGGATGGCA CAGGCTTTGT GGTCTACGAT 660
 GGTGCCGTCT TCTACAACAA GGAGCGCACG CGCAACATCG TCAAGTATGA CCTACGGACG 720
 CGCATCAAGA GCGGGGAGAC GGTTCATCAAT ACCGCCAACC ACCATGACAC CTCGCCCTAC 780
 CGCTGGGGCG GAAAGACCGA CATTGACCTG GCGGTGGACG AGAACGGGCT GTGGGTATC 840
 TACGCCACTG AGGGCAACAA CGGGCGGCTG GTGGTGAACC AGCTGAACCC CTACACACTG 900
 CGCTTTGAGG GCACGTGGGA GACGGGTAC GACAAGCGCT CGGCATCCAA CGCCTTCATG 960
 GTGTGTGGGG TCCTGTACGT CCTGCGCTCC GTGTACGTGG ATGATGACAG CGAGGCGGCT 1020
 GGCAACCGCG TGGACTATGC CTTCAACACC AATGCCAACC GCGAGGAGCC TGTCAGCCTC 1080
 ACCTTCCCCA ACCCTTACCA GTTCATCTCC TCCGTTGACT ACAACCCTCG CGACAACCAAG 1140

CTGTACGTCT	GGAACAAC	TTTCGTGGT	CGCTACAGC	TGGAGTTCG	GCCGCCCCG	1200
CCCAGTGCT	GCCCAGCC	TTCCCCAC	CTCAGCAC	CCACCACAG	CAGGCCACG	1260
CCCCTACCA	GCACAGCT	GCCCCAGC	ACCACCCG	TCCGCCGG	ACCCCTACC	1320
ACGCACCC	TGGGTGCC	CAACCAGCT	GGACCTGAT	TGCCTCCAG	CACAGCCCC	1380
GTCCCCAG	CCCGGCGG	CCCAGCCCC	AATCTACAC	TGTCCCCTG	GCTCTTCTG	1440
GAGCCCCG	AGGTACGG	GGTCCAGTG	CCGGCCACC	AGCAGGGCA	GCTGGTGG	1500
AGGCCCTG	CCAAGGGG	TCGAGGAAT	GCCTCCTTC	AGTGTCTAC	AGCCTTGGG	1560
CTCTGGAAC	CCCGGGGCC	TGACCTCAG	AATGTCAC	CCCCCTGG	CAACCAGGT	1620
GCCCAGAAG	TCAAGAGTG	GGAGAACGC	GCCAACATC	CCAGCGAGC	GGCCCCGAC	1680
ACCCGGGG	CCATCTACG	GGGGGACGT	TCCTCCTCT	TGAAGCTGA	GGAGCAGCT	1740
CTGGACATC	TGGATGCCCC	GCTGCAGGG	CTGCGGCCA	TCGAGCGCG	GTCAGCCGG	1800
AAGAATACA	ACAAGATGA	CAAGCGAG	AGAATTGTA	AGGATTATAT	CAAGGCCGT	1860
GTGGAGAC	TGGACAATC	GCTCCGGCC	GAAGCTCTG	AGTCCTGGA	GGACATGAAT	1920
GCCACGGAG	AGGTGCAC	GGCCACCAT	CTCCTCGAC	TCCTGGAGG	GGGCGCCTT	1980
CTGCTGGCC	ACAATGTC	GGAGCCTGC	CGCTTCCTG	CTGCCAAGG	GAACGTGGT	2040
CTGGAGGTC	CAGTCCTGA	CACAGAGGG	CAGGTGCAG	AGCTGGTGT	CCCCCAGG	2100
GAGTACCC	GAAAGAACT	CATCCAGCT	TCTGCCAAA	CCATCAAGC	GAACAGCCG	2160
AATGGGGTG	TCAAAGTTG	CTTCATCCT	TACAACAAC	TGGGCCTCT	CCTGTCCAC	2220
GAGAATGCC	CAGTGAAGC	GGCCGGCGA	GCAGGCCCG	GTGGCCCTG	GGGCGCCTC	2280
CTAGTGGTG	ACTCACAGG	CATCGCAGC	TCCATCAAC	AGGAGTCC	CCGCGTCTT	2340
CTCATGGAC	CTGTCTCTT	CACCGTGGC	CACCTGGAG	ACAAGAACC	CTTCAATGC	2400
AATGCTCCT	TCTGGAAC	CTCGGAGCG	TCCATGCTG	GCTATTGGT	GACCCAAGG	2460
TGCCGCTGG	TGGAGCCAA	CAAGACCC	ACCAGTGTG	CCTGCAGCC	CCTCACCAC	2520
TTGCGTGTG	TCATGGCTC	CCGTGAGAT	TACCAGGGC	GCATCAACG	GCTGCTGCT	2580
TCGGTTCAT	CCTGGGTGG	CATGTGTAT	TCCCTGGTC	GCTTGGCC	CTGCATCTC	2640
ACCTTCTGT	TCCTGCGGG	GCTGCAGAC	GACCGCAAC	CCATCCACA	GAACCTGTG	2700
ATCAACCTC	TCCTGGCTG	GCTGCTCTT	CTGGTCGGG	TCGACAAG	TCAGTATG	2760
ATTGCCTGC	CCATCTTCG	CGGCCTGTG	CACATTTCT	TCCTGGCTG	CTTCTCCTG	2820
CTGTGCCTG	AGGGCGTGC	CCTCTACCT	CTACTAGTG	AGGTGTTTG	GAGCGAGTA	2880
TCCCGCAC	AGTACTACT	CCTGGGTGG	TACTGCTTC	CGGCCCTGG	GGTGGGCAT	2940
CGGGCTGCC	TTGACTACC	CAGTACCGG	ACCGAGAAG	CCTGCTGGC	CCGAGTGG	3000
AATTACTTC	TCTGGAGTT	CATCGGGCC	GTCTCCTTC	TTATCGTGG	CAACCTGGT	3060
TTCTCATGG	TGACCTGCA	CAAGATGAT	CGAAGCTCA	CTGTGCTCA	GCCCGACTC	3120
AGCCGCTGG	ACAACATT	ATCCTGGGG	CTGGGGGCC	TCGCGCTG	GTTCTCTGT	3180
GGCCTCAC	GGGCTTTTC	CCTCCTCTT	ATCAACAAG	AGTCGGTGG	CATGGCCT	3240
CTCTTCAC	CCTTCAACG	CTTCCAGGG	GTCTTCTAT	TCGTCTTT	CTGCGCCT	3300
CAGAAGAAG	TGCACAAGG	GTACAGCA	TGCCTGCGT	ACTCCTACT	CTGCATCCG	3360
TCCCCACCC	GGGGCACT	CGGATCCCT	AAGACCTCA	CCATGCGA	CAACACCCG	3420
TACTACAC	GGACCCAG	CCGAATTCG	AGGATGTGG	ATGACACTG	GAGGAAAC	3480
ACGGAGTCT	CCTTCATGG	GGGTGACAT	AACAGCACC	CCACCCTGA	CCGAGGTAC	3540
ATGGGGAAC	ACCTGCTG	CAACCCCGT	CTGCAGCCC	GTGGGGGC	CAGTCCCT	3600
AACACCCTC	TCGCCGAG	AGTGGGCTT	AATCCCTCT	CGCCCCCTG	CTTCAACTC	3660
CCAGGGAG	ACCGGGAAC	CAAGCACCC	TTGGGAGGC	GGGAAGCCT	TGGCATGG	3720
ACCCTGCCCC	TGAACGGCA	CTTCAATA	AGTTACTCT	TGCGAAGTG	GGATTTCC	3780
CCCGGGGAT	GGGGCCCTG	GCCGCCCCG	GGCCGGAAC	TAGCCGATG	GGCGGCCCT	3840
GAGAAGATG	TCATCTCAG	GCTGGTGC	AACAACCTG	GGGGGAGC	CAGCGCGGC	3900
AAGGGCCCT	CACCGCCTG	GCCCCCTGT	CCACCTGTG	CAGGGGGCG	GGGCGAGGA	3960
GAGGGGGGG	GGCCCGGGG	TGCTGACCG	GCCGAGATT	AACTTCTCT	TAAGGCCCT	4020
GAGGAGCCT	TGCTGTGCC	CCGGGCCAG	TCGGTGCTG	ACCAGAGCG	TCTGGACG	4080
TCGGAGAGT	GCACGGCCG	GGACGGCGC	ACCAGCCGG	CCCTCTCCT	CCCTCTGGC	4140
CGGGACTCCC	TCTATGCC	CGGGGCCAA	CTGCGGGAC	CACCCTCCT	CCCGACAGC	4200
AGCCCTGAG	GGCCAGTGA	GGCCCTGCCC	CCACCCCTC	CCGCACCCC	CGGCCCCCC	4260
GAAATCTACT	ACACCTCGC	CCCGCCAGC	CTGGTGGCC	GGAATCCC	GCAGGGCT	4320
TACCAGGTG	GGCGTCTAG	CCACGAGGG	TACCTGGC	CCCCAGGC	TGAGGGGCC	4380
GGGCCCCG	GGGACGGCA	GATGCAGCT	GTCACCATC	TC		4425